



# SARS-CoV-2 RT-qPCR Test Detection Rates Are Associated with Patient Age, Sex, and Time since Diagnosis



Matan Levine-Tiefenbrun,<sup>\*</sup> Idan Yelin,<sup>\*</sup> Hedva Uriel,<sup>†</sup> Jacob Kuint,<sup>‡§</sup> Licitia Schreiber,<sup>¶</sup> Esmā Herzeli,<sup>‡</sup> Rachel Katz,<sup>‡</sup> Amir Ben-Tov,<sup>‡§</sup> Sivan Gazit,<sup>‡</sup> Tal Patalon,<sup>‡</sup> Gabriel Chodick,<sup>‡§</sup> and Roy Kishony<sup>\*†</sup>

From the Biology Faculty<sup>\*</sup> and the Faculty of Computer Science,<sup>†</sup> Technion—Israel Institute of Technology, Haifa; the Maccabitech,<sup>‡</sup> Maccabi Health Services, Tel Aviv; the Sackler Faculty of Medicine,<sup>§</sup> Tel-Aviv University, Tel-Aviv; and the Maccabi Megalab,<sup>¶</sup> Maccabi Healthcare Services, Rehovot, Israel

Accepted for publication  
October 4, 2021.

Address correspondence to Idan Yelin, Ph.D., Faculty of Biology, Technion—Israel Institute of Technology, Haifa 320003, Israel. E-mail: [idany@technion.ac.il](mailto:idany@technion.ac.il).

Quantifying the detection rate of the widely used quantitative RT-PCR (RT-qPCR) test for severe acute respiratory syndrome coronavirus 2 and its dependence on patient demographic characteristics and disease progression is key in designing epidemiologic strategies. Analyzing 843,917 test results of 521,696 patients, a “positive period” was defined for each patient between diagnosis of coronavirus disease 2019 and the last positive test result. The fraction of positive test results within this period was then used to estimate detection rate. Regression analyses were used to determine associations of detection with time of sampling after diagnosis, patient demographic characteristics, and viral RNA copy number based on RT-qPCR cycle threshold values of the next positive test result. The overall detection rate in tests performed within 14 days after diagnosis was 83.1%. This rate was higher at days 0 to 5 after diagnosis (89.3%). Furthermore, detection rate was strongly associated with age and sex. Finally, the detection rate with the Allplex 2019-nCoV RT-qPCR kit was associated, at the single-patient level, with viral RNA copy number ( $P < 10^{-9}$ ). These results show that the reliability of the test result is reduced in later days as well as for women and younger patients, in whom the viral loads are typically lower. (*J Mol Diagn* 2022, 24: 112–119; <https://doi.org/10.1016/j.jmoldx.2021.10.010>)

The ongoing coronavirus disease 2019 (COVID-19) pandemic has already infected tens of millions of individuals worldwide. A major tool in combating the pandemic is testing for viral carriage, which is used for both diagnostic and epidemiologic purposes. The most commonly used viral detection tests are based on quantitative RT-PCR (RT-qPCR) of viral genes. This nucleic acid test is of high specificity (ie, very low false-positive rate).<sup>1–4</sup> In contrast, the false-negative rate of these tests has often been reported as high.<sup>5–9</sup> High false-negative rates may impede local and global efforts to slow down disease spread, as patients incorrectly diagnosed as noncarriers might pose an obstacle for efforts such as contact tracing.<sup>10–12</sup> Systematically quantifying the rate of detection and its dependencies on disease progression and patient demographic characteristics is therefore critical for disease spread modeling and public health policy-making.

Various approaches have been taken to estimate the false-negative rate of COVID-19 RT-qPCR tests. Measuring the rate of false-negative results in a population of patients with highly specific pathologies (eg, chest CT imaging) has initially alerted physicians and epidemiologists of the high false-negative rate, estimated at approximately 30%.<sup>3–6,8,13–16</sup> A meta-analysis of multiple such studies found that the reported rates were highly variable, with a mean false-negative rate of 11%.<sup>17</sup> However, and as noted previously,<sup>17,18</sup> these meta-analysis studies were necessarily based on a combination of variable studies of nonuniform

Supported by the Israel Science Foundation (grant 3633/19 to R.Ki. and G.C.) within the KillCorona—Curbing Coronavirus Research Program. The funding source was not involved in the writing of the manuscript.

M.L.-T., I.Y., and H.U. contributed equally to this work.

Disclosures: None declared.

origins and methodologies, using different kits with inherently different limits of detection and typically involving small groups of patients. Another approach compared initial RT-qPCR test results versus post hoc convalescent serologic test results, finding a false-negative rate of 14%.<sup>19</sup> A more recent systematic approach was based on “longitudinal testing” in which the accuracy of each test is determined based on later tests of the same patient: a negative test result that is soon followed by a positive one is deemed false negative.<sup>20,21</sup> Application of this approach in a hospital setting resulted in an estimation of a false-negative rate of 17.8%.<sup>18</sup>

Beyond the average false-negative rate, meta-analysis studies showed a strong association of false-negative results with time since exposure<sup>22</sup> or time since onset of symptoms.<sup>23</sup> These associations suggest that negative test results obtained during a “positive period” reflect waning infections and viral loads declining toward the test limit of detection. Therefore, such negative results do not necessarily indicate a false-negative result, especially as later positive results may be of high cycle threshold ( $C_T$ ) values and may result from fragmented RNA and not from infectious viral particles.<sup>24</sup> Moreover, at the patient-specific level, because the viral load is associated with time since onset of symptoms, sex, and age,<sup>25–33</sup> it has been proposed that detection rates might also depend on demographic characteristics; however, current studies lacked statistical power for quantifying such dependencies.<sup>18,34–39</sup>

Here, using a large data set of quantitative patient-level test series performed with a single type of measurement equipment with a characterized limit of detection [Hur et al,<sup>16</sup> and the Allplex 2019-vCoV Assay, version 2.2 (see manufacturer’s instructions; Seegene, Inc., Seoul, South Korea)], with linked demographic characteristics and electronic health records (843,917 tests for 521,969 patients), a longitudinal testing–based approach was applied to quantify the detection rate of COVID-19 test results at the community level and its associations with age, sex, and time since diagnosis. Finally, we tested whether this rate is associated with viral RNA copy number at the single-patient level.

## Materials and Methods

### Ethical Approval

The study protocol was approved by the ethics committee of Maccabi Healthcare Services, Tel-Aviv, Israel (institutional review board number: 0066-20-MHS).

### Data Collection

Anonymized clinical records of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RT-qPCR test results (test reports) were retrieved by Maccabi Healthcare Services (MHS) for the period between February 8, 2020, and September 24, 2020. Records of COVID-19 or COVID-19–related diagnoses by physicians (diagnosis reports)

were retrieved for these patients. When available,  $C_T$  values of the PCR test were retrieved for each test (ie, RT-qPCR measurements). Randomly generated identifiers were used to link between test results and diagnosis codes.

### Test Results

MHS aggregates all test results for all its members, regardless of whether the test itself was performed by the MHS laboratory. Test results data included, for each test, the following: random patient number, sample number, sample execution date, and test result. Test results were either “positive” (7.4%), “negative” (92%), or “borderline-positive” (0.6%, which were considered as positive in the analysis). Patients for whom two tests with different results were recorded on the same day were excluded from the analysis [274 patients (0.05%)].

### Diagnosis Reports

Diagnoses are routinely recorded in the MHS database. For all patients with at least one positive test result, any symptom-based COVID-19 diagnoses recorded before their first test were retrieved. Diagnosis report data included random patient number, diagnosis date, and diagnosis code (International Classification of Diseases, Ninth Revision, and internal MHS codes).

### RT-qPCR Measurements

For each test, the following data were included: sample number, PCR machine number, test well number, test date, and  $C_T$  values for four channels (FAM, Cal Red 610, Quasar 670, and HEX, corresponding to the measurements of *E* gene, *RdRp* gene, *N* gene, and the internal control, respectively).  $C_T$  values were calculated similarly for all genes using Seegene proprietary software for the Allplex 2019-nCoV assay (Seegene) after collection of oro-nasopharyngeal swab specimens.

### Assigning Patient Diagnosis Date

For each patient, the earliest date of COVID-19 symptoms and/or epidemiologically based referral was considered as “date of diagnosis.” When both symptom-based diagnosis and epidemiologic-based referrals were available, they were usually recorded on the same day. For simplicity, a small number of patients for whom both a diagnosis and a referral were available but were more than 1 day apart were excluded (5.2% of diagnosed patients).

### Calculating the Detection Rate

For any patient with at least one positive test result, a “positive period” was defined as the period between their date of diagnosis and their last positive test result. Negative test reports during this period were regarded as undetectable, whereas positive test reports during this period were regarded as detectable. Detection rate was calculated as: Detectable/(Detectable + UnDetectable).

## Logistic Regression

Logistic regression of an undetectable result versus a detectable result was performed by using the Python statsmodels library. The probability of a detectable result was fitted to the test result (detectable, 1; undetectable, 0) for all tests within the positive period.

## Linear Regression

Linear regression of  $C_T$  values for each fluorescence channel was performed by using the Python statsmodels library.

## Calculating Odds Ratios from Logistic Regression

Odds ratios (ORs) were calculated from the coefficients of the aforementioned logistic regression. For the binary variable sex (male, 1; female, 0), OR was defined as:  $OR_{sex} = \exp(C_{sex})$ . For the continuous variables age and day, ORs were defined as:  $\exp(C_{age} \times age_{older} - C_{age} \times age_{younger})$  younger versus older,  $\exp(C_{day} \times day_{early} - C_{day} \times day_{late})$  early versus late, where  $C_{sex}$ ,  $C_{day}$ ,  $C_{age}$  are the coefficients for the sex, day, and age variables, respectively.

## Differences in Detection Rate between Age Groups

Test results were divided into two groups of similar size according to patient age (<40 years and  $\geq$ 40 years). Detection rate was calculated separately for each group. Statistical significance for differences in detection rate between groups was tested by using a two-sided Fisher's exact test (SciPy in Python).

## Results

### Building a Large Longitudinal COVID-19 Test Data Set

Among all approximately 2 million MHS patients, 843,917 recorded tests were identified for 521,696 patients. Within this set, 51,499 patients had at least one positive result. Because quarantine discharge policy was based on test results, patients were often repeatedly tested, resulting in a series of test results for each patient. The analysis focused on 7858 patients with well-defined test series, satisfying the following conditions: i) had a defined diagnosis date with COVID-19 symptoms; ii) had at least one positive sample within 14 days after the diagnosis date; and iii) had a test series that ended with a negative result (Table 1). The majority of these test series ended with two or more negative results, in agreement with the discharge policy (68% of patients) (Supplemental Table S1).

### Identifying Undetectable and Detectable Test Results

Undetectable and detectable test results were defined based on their context within a patient series of test results. For each patient, the series of test results after diagnosis were

considered (Figure 1, A and B). The median day since diagnosis until the first negative result, indicating recovery, was 18 (interquartile range, 13-24 days) (Table 1). For few patients, a negative result came only after >50 days (2.5% of patients). For each patient, the period from diagnosis date to the last positive sample was then considered as a period in which the patient was carrying viral RNA fragments, even if not yet at detectable loads (ie, the positive period). Taking an epidemiologic stand, only negative results outside of the positive period were regarded as negative, whereas negative test results within this patient-specific positive time period were regarded as undetectable results. Similarly, positive test results within this period were regarded as detectable (Figure 1A). To avoid bias for detectable results, the last positive result, used for defining the end of the positive period, was not counted toward detectable results. The rate of negative results increased over time, and at 20 days after diagnosis, the number of negative test results first surpassed the number of positive or undetectable results (Figure 1, B and C). Relative to time of the first negative test result, undetected test results were extremely rare during the two preceding days but were otherwise relatively equally distributed, indicating that undetectable test results were not restricted to the short time period of the end of carriage (Supplemental Figure S1). Focusing on days 0 to 14 after diagnosis, representing the typical duration of the disease, 1047 test results defined as undetectable and 5143 test results defined as detectable were identified, indicating an overall detection rate of 83.1%.

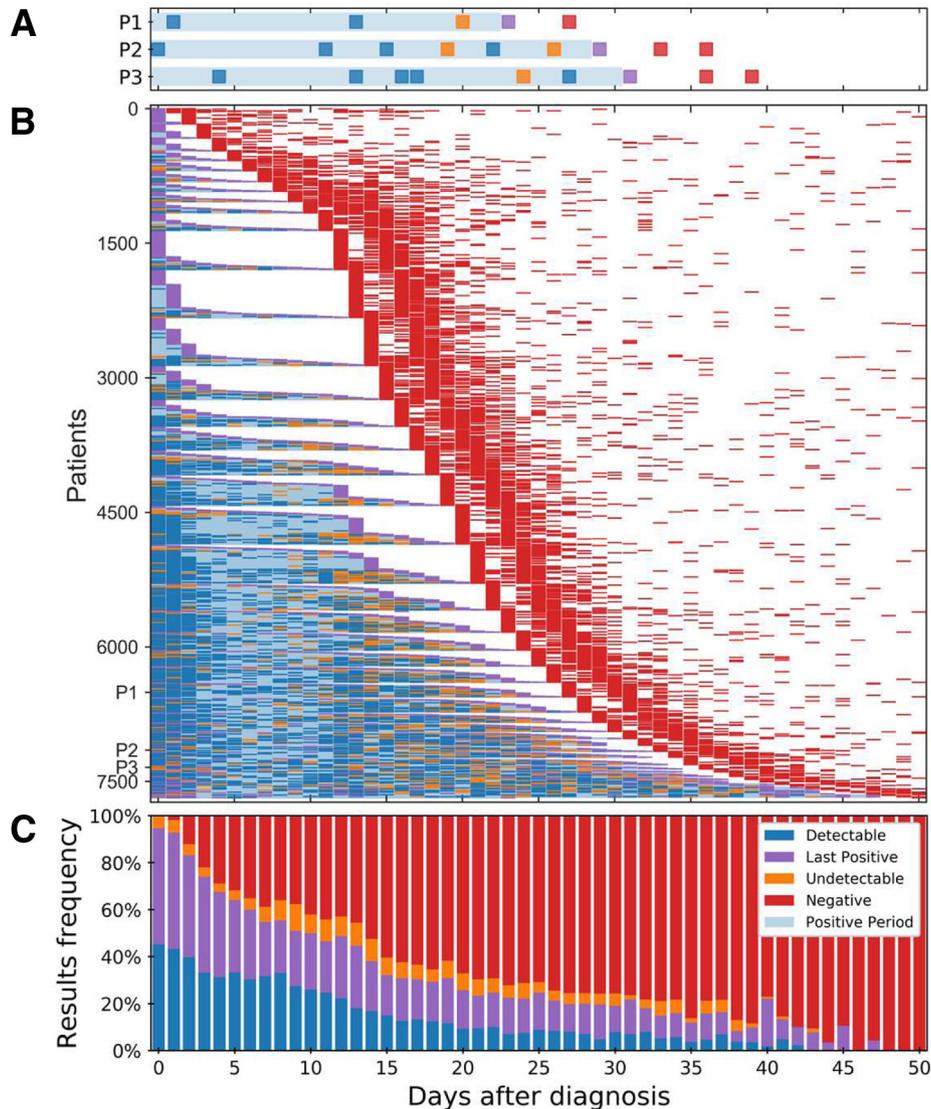
### Age, Sex, and Time after Diagnosis Are Associated with Detection Rate

To identify personalized features associated with detection rate, multivariate logistic regression for the odds of an

**Table 1** Study Population Characteristics

Characteristic	Study population (N = 7858)
Age, years	
Mean $\pm$ SD	36.75 $\pm$ 20.18
Distribution, no. (%)	
<40 years	4391 (55.88)
$\geq$ 40 years	3467 (44.12)
Sex, no. (%)	
Male	4156 (52.89)
Female	3702 (47.11)
Test result, no. (%)	
Positive	14,559 (45.46)
Negative	17,466 (54.54)
Median positive period length (IQR), days	5 (1 to 16)
Median time to recovery (IQR), days	18 (13 to 24)
Median test series length (IQR), days	22 (16 to 30)

IQR, interquartile range.

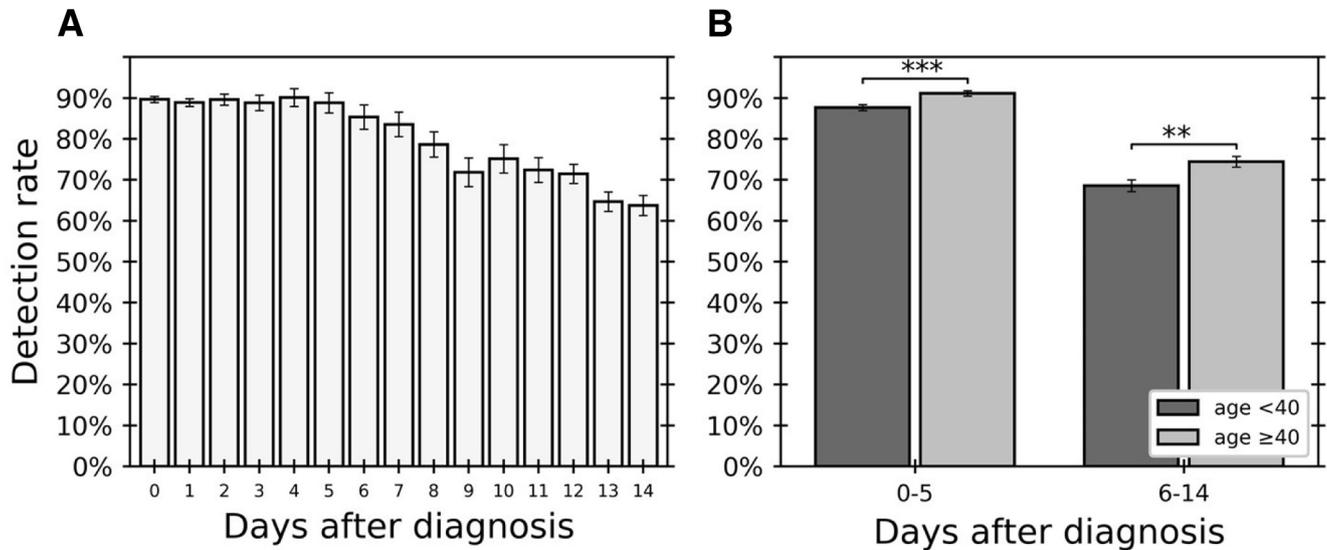


**Figure 1** Longitudinal quantitative RT-PCR severe acute respiratory syndrome coronavirus 2 test results for patients diagnosed with coronavirus disease 2019. **A:** Test results for three representative patients (P1, P2, and P3). The day of diagnosis and the last positive test result (purple) demarcate the “positive period” (light blue shading). Negative test results within this individually determined period were regarded as “undetectable” (orange). Similarly, positive test results within the positive period were regarded as detectable (blue). All test series end with a sequence of one or more negative results (red). **B:** Longitudinal severe acute respiratory syndrome coronavirus 2 test results for the study population (Table 1). [For clarity, 191 patients for whom the first negative sample (red) was obtained >50 days after the day of diagnosis were omitted.] Patients are sorted according to the dates, relative to diagnosis, of their first negative result, then by the relative date of the last positive result. **C:** Frequency of test results per day relative to diagnosis.

undetectable versus detectable result was performed (as discussed in *Logistic Regression* and *Calculating Odds Ratios from Logistic Regression*). Patient age, sex, and number of days since diagnosis were all associated with an undetectable result (Supplemental Table S2). Patient age was strongly anticorrelated with an undetectable result, with an OR of 1.36 (95% CI, 1.34 to 1.39) for patients 10 years younger. The number of days from diagnosis was positively correlated with an undetectable result, with an OR of 1.98 (95% CI, 1.78 to 2.20) for samples taken at day 14 compared with samples taken at day 0. Lastly, patient sex was also strongly associated with undetectable results, with a female to male OR of 1.73 (95% CI, 1.58 to 1.9).

Following the observed association between time after diagnosis and detectable result, the detection rate during disease progression was characterized. Calculating detection rate per day after diagnosis (as discussed in *Calculating the Detection Rate*), that detection rate during the first few days was found to be fairly constant and high (89.3%, days 0 to 5) and to then gradually decrease over days 6 to 14 (Figure 2A).

The earlier days after diagnosis (days 0 to 5), in which the detection rate was relatively high, and in which a precise diagnosis is most critical for epidemiologic needs and contact tracing were further studied. Multivariate logistic regression analysis of test results for these days



**Figure 2** Detection rate changes along time after day of diagnosis and differs between age groups. Detection rate per day after diagnosis was calculated for 6190 tests. **A:** Daily detection rate for days between day of diagnosis (day 0) to 14 days after diagnosis. **B:** Difference in detection rate between two age groups (<40 years and  $\geq 40$  years [dark and light gray, respectively]) calculated separately for early and late days after diagnosis. Fisher's exact test (as discussed in [Differences in Detection Rate between Age Groups](#)) was used. Error bars indicate SD.  $**P < 0.01$ ,  $***P < 0.001$ .

alone identified an association of undetectable results during these days with sex and age. The risk of undetectable result was again associated with age (OR of 1.56 for patients 10 years younger; 95% CI, 1.51 to 1.61), and sex (female to male OR of 2.02; 95% CI, 1.70 to 2.40) ([Supplemental Table S3](#)). Dividing the patients into two age groups of similar size (those aged <40 years and  $\geq 40$  years) ([Table 1](#)), the detection rate during this initial period was found to be significantly lower for the younger age group ( $P = 0.0004$ , Fisher's exact test; OR, 0.72; 95% CI, 0.59 to 0.88) ([Figure 2B](#)). Similarly, the detection rate during the later period (days 6 to 14) also significantly increased with age ( $P = 0.003$ , Fisher's exact test).

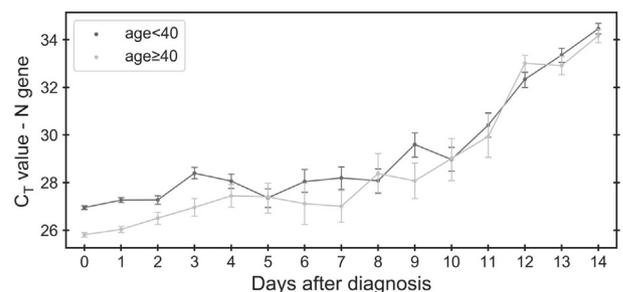
### Age, Sex, and Time after Diagnosis Are Associated with Viral RNA Copy Number Similarly to Detection Rate

Based on previous reports of viral load differences between male subjects and female subjects, among age groups and along disease progression,<sup>4,25–28,30,40–46</sup> we hypothesized that differences in detection rate across demographic factors and disease progression may stem from changes in viral load, which would be reflected in the measured  $C_T$  values. To test this hypothesis, associations of  $C_T$  values of the three viral genes (*N*, *E*, and *RdRp*) and the internal control gene were studied with patient age and sex and with number of days after diagnosis ([Figure 3](#) and [Supplemental Figure S2](#)). Indeed, a linear regression model revealed positive correlation of the  $C_T$  of viral genes with the number of days after diagnosis, and negative correlation with age and sex (male; as discussed in [Linear Regression](#)) ([Supplemental](#)

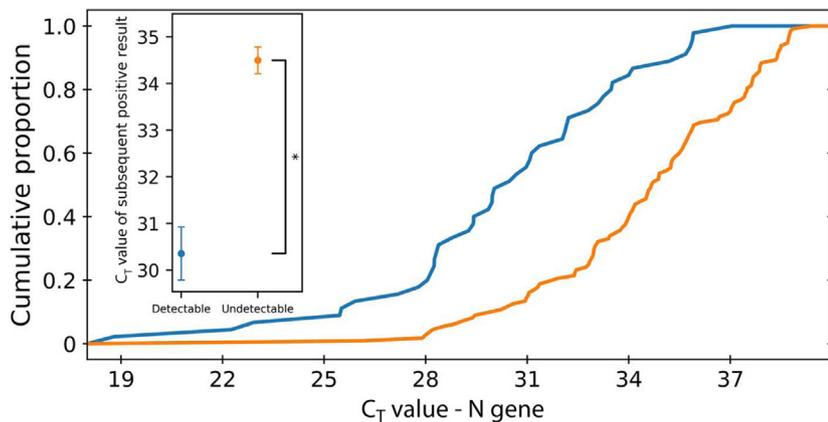
[Table S4](#)). An opposite association was found with the internal control gene, in agreement with within-tube competition for reagents between the multiplexed reactions ([Supplemental Figure S2C](#)).<sup>47</sup> The viral RNA copy number association with demographic characteristics and time therefore mirrored the associations of the detection rate with these same parameters.

### Viral RNA Copy Number and Detection Rate Are Associated at the Individual Patient Level

Finally, an association of detection rate with viral RNA copy number at the individual patient level was tested. Because  $C_T$  values are, by definition, not available for undetectable results, the  $C_T$  values of the next positive result were used as a proxy (provided that such a sample existed within the 14 days after diagnosis). Comparing the distribution of  $C_T$  values of positive test results after undetectable



**Figure 3** Differential change in cycle threshold ( $C_T$ ) value of the *N* gene along time after day of diagnosis for different age groups. In the first 4 days after diagnosis,  $C_T$  values of the *N* gene are lower for older patients (age  $\geq 40$  years, light gray) than for younger patients (age <40 years, dark gray). Error bars indicate SEM.



**Figure 4** Difference between cycle threshold ( $C_T$ ) values of the  $N$  gene of positive results after undetectable and detectable test. Positive test results that followed an undetectable test result have a higher  $C_T$  value than positive test results after undetectable test results. Error bars indicate SEM.  $*P < 10^{-10}$ .

results versus the  $C_T$  values of positive test results after detectable results, it was found that undetectable results were indeed associated with reduced viral RNA copy number for all three viral genes (Mann-Whitney  $U$  test;  $P$ -values of  $1.65 \times 10^{-9}$ ,  $1.03 \times 10^{-9}$ , and  $8.99 \times 10^{-10}$  for  $N$ ,  $E$ , and  $RdRp$  genes, respectively) (Figure 4 and Supplemental Figure S3). Importantly, these  $C_T$  values, despite being higher, were on average well below the limit of detection and within the observed  $C_T$  distribution of each gene (Figure 4, inset, and Supplemental Figure S4).

## Discussion

The current analysis of a large data set of electronic health records of patients with COVID-19 showed that although, on average, the detection rate is about 83%, this rate varies strongly with age, sex, and time after diagnosis. At the first few days after diagnosis, the detection rate is only 90% on average and even higher for men and older patients. Combining these data with  $C_T$  values of RT-qPCR tests provides evidence that detection rates possibly stem from low viral loads at the single-patient level.

The study has several limitations. First, all positive test results are treated as true positives. Although errors may occur, the rate of false-positive results is very low<sup>1-4</sup> and is not expected to significantly affect results. Future studies can further improve the reliability of confirmation of positive cases by combining PCR test results with serology test results. Second, negative results at the end of test series are treated as “true negative” and not an undetectable result, whereas it is possible that if further tests were performed, additional positive tests might have been detected. Again, this is not expected to significantly affect results as most series in this study end with two consecutive negative results. Moreover, this bias will mostly affect the calculated detection rate at later days after diagnosis. Third, because viral loads after infection may first increase and only later decrease,<sup>4,26,41,46</sup> it is possible that detection rates follow a similar pattern: first increasing and only later decreasing. Analyzing the cohort, only the later phase of the decreasing

detection rate could be identified. However, it is possible that with different cohorts or inclusion criteria, the earlier phase of decreasing viral load and increasing detection rate can also be observed. Fourth, despite all samples with  $C_T$  values being treated in the same central facility, which increases the uniformity of the data set, multiple other factors such as the type of swab and swab transport conditions (eg, time, temperature), as well as operator-dependent factors regarding sample collection and handling, can affect test sensitivity. These factors are not recorded and are therefore not included in our analysis. Fifth, because the beginning of the positive period is based on the date of diagnosis, it does not directly represent the onset of disease. However, it is the best available proxy for it. Finally, this study was limited to unvaccinated symptomatic patients; therefore, these results may not represent the detection rate for asymptomatic or vaccinated patients for whom viral load may be lower.<sup>48,49</sup>

Despite these limitations, these results provide important epidemiologic input as to the patient-specific sensitivity of tests, with important implications for epidemiologic policy-making, contact tracing, and disease prevention and control. The results underscore that the risk of an undetectable infection at the very early days after diagnosis might be lower than previously thought, reinforcing the usefulness of these tests for epidemiologic decisions.

## Author Contributions

M.L.-T., I.Y., T.P., G.C., and R.Ki. designed the study; I.Y., L.S., E.H., and R.Ka. collected data; M.L.-T., I.Y., H.U., and R.Ki. analyzed data; M.L.-T., I.Y., H.U., J.K., L.S., A.B.-T., T.P., S.G., G.C., and R.Ki. interpreted data; M.L.-T., I.Y., H.U., and R.Ki. wrote the manuscript, with comments from all authors.

## Supplemental Data

Supplemental material for this article can be found at <http://doi.org/10.1016/j.jmoldx.2021.10.010>.

## References

1. Bisoffi Z, Pomari E, Deiana M, Piubelli C, Ronzoni N, Beltrame A, Bertoli G, Riccardi N, Perandin F, Formenti F, Gobbi F, Buonfrate D, Silva R: Sensitivity, specificity and predictive values of molecular and serological tests for COVID-19: a longitudinal study in emergency room. *Diagnostics (Basel)* 2020, 10:669
2. Pfefferle S, Reucher S, Nörz D, Lütgehetmann M: Evaluation of a quantitative RT-PCR assay for the detection of the emerging coronavirus SARS-CoV-2 using a high throughput system. *Euro Surveill* 2020, 25:2000152
3. Wu SL, Mertens AN, Crider YS, Nguyen A, Pokpongkiat NN, Djajadi S, Seth A, Hsiang MS, Colford JM Jr, Reingold A, Arnold BF, Hubbard A, Benjamin-Chung J: Substantial underestimation of SARS-CoV-2 infection in the United States. *Nat Commun* 2020, 11:4507
4. Wölfel R, Corman VM, Guggemos W, Seilmaier M, Zange S, Müller MA, Niemeyer D, Jones TC, Vollmar P, Rothe C, Hoelscher M, Bleicker T, Brünink S, Schneider J, Ehmann R, Zwirgmaier K, Drosten C, Wendtner C: Virological assessment of hospitalized patients with COVID-2019. *Nature* 2020, 581:465–469
5. Xie X, Zhong Z, Zhao W, Zheng C, Wang F, Liu J: Chest CT for typical coronavirus disease 2019 (COVID-19) pneumonia: relationship to negative RT-PCR testing. *Radiology* 2020, 296:E41–E45
6. Ai T, Yang Z, Hou H, Zhan C, Chen C, Lv W, Tao Q, Sun Z, Xia L: Correlation of chest CT and RT-PCR testing for coronavirus disease 2019 (COVID-19) in China: a report of 1014 cases. *Radiology* 2020, 296:E32–E40
7. Di Paolo M, Iacovelli A, Olmati F, Menichini I, Oliva A, Carnevalini M, Graziani E, Mastroianni CM, Palange P: False-negative RT-PCR in SARS-CoV-2 disease: experience from an Italian COVID-19 unit. *ERJ Open Res* 2020, 6:00324-2020
8. Yang Y, Yang M, Yuan J, Wang F, Wang Z, Li J, Zhang M, Xing L, Wei J, Peng L, Wong G, Zheng H, Wu W, Shen C, Liao M, Feng K, Li J, Yang Q, Zhao J, Liu L, Liu Y: Laboratory diagnosis and monitoring the viral shedding of SARS-CoV-2 infection. *Innovation (N Y)* 2020, 1:100061
9. Zhang J-F, Yan K, Ye H-H, Lin J, Zheng J-J, Cai T: SARS-CoV-2 turned positive in a discharged patient with COVID-19 arouses concern regarding the present standards for discharge. *Int J Infect Dis* 2020, 97:212–214
10. Woloshin S, Patel N, Kesselheim AS: False negative tests for SARS-CoV-2 infection—challenges and implications. *N Engl J Med* 2020, 383:e38
11. Çubukçu HC, Coşkun A: False negative results and tolerance limits of SARS-CoV-2 laboratory tests. *Pathog Glob Health* 2021, 115: 137–138
12. Watson J, Whiting PF, Brush JE: Interpreting a covid-19 test result. *BMJ* 2020, 369:m1808
13. Kohli A, Joshi A, Shah A, Jain RD, Gorlawar A, Dhapare A, Desai J, Shetty A, Shah C, Ostwal P, Talraja A: Does CT help in reducing RT-PCR false negative rate for COVID-19? *Indian J Radiol Imaging* 2021, 31(Suppl 1):S80–S86
14. Wang L, Liu X, Xia C, Liu J, Zhou X-H: More accurate estimates of the accuracy of RT-PCR and chest CT tests for COVID-19. *Res Square* 2021, [Preprint] doi: 10.21203/rs.3.rs-182065/v1
15. Reich N, Lowe CF, Puddicombe D, Matic N, Greiner J, Simons J, Leung V, Chu T, Naik H, Myles N, Burns L, Romney MG, Ritchie G, Champagne S, Dooley K, Sekirov I, Stefanovic A: Diagnostic accuracy of RT-PCR for detection of SARS-CoV-2 compared to a “composite reference standard” in hospitalized patients. *medRxiv* 2021, [Preprint] doi: 10.1101/2021.02.18.21252016
16. Hur K-H, Park K, Lim Y, Jeong YS, Sung H, Kim M-N: Evaluation of four commercial kits for SARS-CoV-2 real-time reverse-transcription polymerase chain reaction approved by emergency-use-authorization in Korea. *Front Med (Lausanne)* 2020, 7:521
17. Kim H, Hong H, Yoon SH: Diagnostic performance of CT and reverse transcriptase polymerase chain reaction for coronavirus disease 2019: a meta-analysis. *Radiology* 2020, 296:E145–E155
18. Williams TC, Wastnedge E, McAllister G, Bhatia R, Cuschieri K, Kefala K, Hamilton F, Johannessen I, Laurenson IF, Shepherd J, Stewart A, Waters D, Wise H, Templeton KE: Sensitivity of RT-PCR testing of upper respiratory tract samples for SARS-CoV-2 in hospitalised patients: a retrospective cohort study. *Wellcome Open Res* 2020, 5:254
19. Holborow A, Asad H, Porter L, Tidswell P, Johnston C, Blyth I, Bone A, Healy B: The clinical sensitivity of a single SARS-CoV-2 upper respiratory tract RT-PCR test for diagnosing COVID-19 using convalescent antibody as a comparator. *Clin Med (Lond)* 2020, 20:e209–e211
20. Thompson EE, Rosenthal J, Wren J, Seetao E, Olson NH: Repeated testing necessary: assessing negative predictive value of SARS-CoV-2 qPCR in a population of young adults. *bioRxiv* 2021, [Preprint] doi: 10.1101/2021.03.10.21253292
21. Kanji JN, Zelyas N, MacDonald C, Pabbaraju K, Khan MN, Prasad A, Hu J, Diggle M, Berenger BM, Tipples G: False negative rate of COVID-19 PCR testing: a discordant testing analysis. *Virol J* 2021, 18:13
22. Kucirka LM, Lauer SA, Laeyendecker O, Boon D, Lessler J: Variation in false-negative rate of reverse transcriptase polymerase chain reaction-based SARS-CoV-2 tests by time since exposure. *Ann Intern Med* 2020, 173:262–267
23. Wikramaratna PS, Paton RS, Ghafari M, Lourenço J: Estimating the false-negative test probability of SARS-CoV-2 by RT-PCR. *Euro Surveill* 2020, 25:2000568
24. Jefferson T, Spencer EA, Brassey J, Heneghan C: Viral cultures for coronavirus disease 2019 infectivity assessment: a systematic review. *Clin Infect Dis* 2021, 73:e3884–e3899
25. To KK-W, Tsang OT-Y, Leung W-S, Tam AR, Wu T-C, Lung DC, Yip CC-Y, Cai J-P, Chan JM-C, Chik TS-H, Lau DP-L, Choi CY-C, Chen L-L, Chan W-M, Chan K-H, Ip JD, Ng AC-K, Poon RW-S, Luo C-T, Cheng VC-C, Chan JF-W, Hung IF-N, Chen Z, Chen H, Yuen K-Y: Temporal profiles of viral load in posterior oropharyngeal saliva samples and serum antibody responses during infection by SARS-CoV-2: an observational cohort study. *Lancet Infect Dis* 2020, 20:565–574
26. He X, Lau EHY, Wu P, Deng X, Wang J, Hao X, Lau YC, Wong JY, Guan Y, Tan X, Mo X, Chen Y, Liao B, Chen W, Hu F, Zhang Q, Zhong M, Wu Y, Zhao L, Zhang F, Cowling BJ, Li F, Leung GM: Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med* 2020, 26:672–675
27. Yonker LM, Neilan AM, Bartsch Y, Patel AB, Regan J, Arya P, Gootkind E, Park G, Hardcastle M, St. John A, Appleman L, Chiu ML, Fialkowski A, De la Flor D, Lima R, Bordt EA, Yockey LJ, D’Avino P, Fischinger S, Shui JE, Lerou PH, Bonventre JV, Yu XG, Ryan ET, Bassett IV, Irimia D, Edlow AG, Alter G, Li JZ, Fasano A: Pediatric severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): clinical presentation, infectivity, and immune responses. *J Pediatr* 2020, 227:45–52.e5
28. Jones TC, Biele G, Mühlemann B, Veith T, Schneider J, Beheim-Schwarzbach J, Bleicker T, Tesch J, Schmidt ML, Sander LE, Kurth F, Menzel P, Schwarzer R, Zuchowski M, Hofmann J, Krumbholz A, Stein A, Edelmann A, Corman VM, Drosten C: Estimating infectiousness throughout SARS-CoV-2 infection course. *Science* 2021, 373:eabi5273
29. Lennon NJ, Mina M, Rehm HL, Hung DT, Smole S, Woolley AE, Lander E, Gabriel S: LB-11. Comparison of viral loads in individuals with or without symptoms at time of COVID-19 testing among 32,480 residents and staff of nursing homes and assisted living facilities in Massachusetts. *Open Forum Infect Dis* 2020, 7:S848–S849
30. Walsh KA, Jordan K, Clyne B, Rohde D, Drummond L, Byrne P, Ahern S, Carty PG, O’Brien KK, O’Murchu E, O’Neill M, Smith SM, Ryan M, Harrington P: SARS-CoV-2 detection, viral load

- and infectivity over the course of an infection. *J Infect* 2020, 81: 357–371
31. Shi F, Wu T, Zhu X, Ge Y, Zeng X, Chi Y, Du X, Zhu L, Zhu F, Zhu B, Cui L, Wu B: Association of viral load with serum biomarkers among COVID-19 cases. *Virology* 2020, 546:122–126
  32. Alidjinou EA, Poissy J, Ouafi M, Caplan M, Benhalima I, Goutay J, Tinez C, Faure K, Chopin M-C, Yelnik C, Lambert M, Hober D, Preau S, Nseir S, Engelmann I: on behalf of the Lille Covid Research Network Licorne: Spatial and temporal virus load dynamics of SARS-CoV-2: a single-center cohort study. *Diagnostics (Basel)* 2021, 11:427
  33. Mahallawi WH, Alsamiri AD, Dabbour AF, Alsaedi H, Al-Zalabani AH: Association of viral load in SARS-CoV-2 patients with age and gender. *Front Med (Lausanne)* 2021, 8:608215
  34. Xiao AT, Tong YX, Gao C, Zhu L, Zhang YJ, Zhang S: Dynamic profile of RT-PCR findings from 301 COVID-19 patients in Wuhan, China: a descriptive study. *J Clin Virol* 2020, 127:104346
  35. Arevalo-Rodriguez I, Buitrago-Garcia D, Simancas-Racines D, Zambrano-Achig P, Del Campo R, Ciapponi A, Sued O, Martinez-García L, Rutjes AW, Low N, Bossuyt PM, Perez-Molina JA, Zamora J: False-negative results of initial RT-PCR assays for COVID-19: a systematic review. *PLoS One* 2020, 15:e0242958
  36. Zhang J-J, Cao Y-Y, Dong X, Wang B-C, Liao M-Y, Lin J, Yan Y-Q, Akdis CA, Gao Y-D: Distinct characteristics of COVID-19 patients with initial rRT-PCR-positive and rRT-PCR-negative results for SARS-CoV-2. *Allergy* 2020, 75:1809–1812
  37. Fang Y, Zhang H, Xie J, Lin M, Ying L, Pang P, Ji W: Sensitivity of chest CT for COVID-19: comparison to RT-PCR. *Radiology* 2020, 296:E115–E117
  38. Li Y, Yao L, Li J, Chen L, Song Y, Cai Z, Yang C: Stability issues of RT-PCR testing of SARS-CoV-2 for hospitalized patients clinically diagnosed with COVID-19. *J Med Virol* 2020, 92:903–908
  39. Xiao AT, Tong YX, Zhang S: False negative of RT-PCR and prolonged nucleic acid conversion in COVID-19: rather than recurrence. *J Med Virol* 2020, 92:1755–1756
  40. Pan Y, Zhang D, Yang P, Poon LLM, Wang Q: Viral load of SARS-CoV-2 in clinical samples. *Lancet Infect Dis* 2020, 20:411–412
  41. Zou L, Ruan F, Huang M, Liang L, Huang H, Hong Z, Yu J, Kang M, Song Y, Xia J, Guo Q, Song T, He J, Yen H-L, Peiris M, Wu J: SARS-CoV-2 viral load in upper respiratory specimens of infected patients. *N Engl J Med* 2020, 382:1177–1179
  42. Huang Y, Chen S, Yang Z, Guan W, Liu D, Lin Z, Zhang Y, Xu Z, Liu X, Li Y: SARS-CoV-2 viral load in clinical samples from critically ill patients. *Am J Respir Crit Care Med* 2020, 201:1435–1438
  43. Liu W-D, Chang S-Y, Wang J-T, Tsai M-J, Hung C-C, Hsu C-L, Chang S-C: Prolonged virus shedding even after seroconversion in a patient with COVID-19. *J Infect* 2020, 81:318–356
  44. Zheng S, Fan J, Yu F, Feng B, Lou B, Zou Q, Xie G, Lin S, Wang R, Yang X, Chen W, Wang Q, Zhang D, Liu Y, Gong R, Ma Z, Lu S, Xiao Y, Gu Y, Zhang J, Yao H, Xu K, Lu X, Wei G, Zhou J, Fang Q, Cai H, Qiu Y, Sheng J, Chen Y, Liang T: Viral load dynamics and disease severity in patients infected with SARS-CoV-2 in Zhejiang province, China, January-March 2020: retrospective cohort study. *BMJ* 2020, 369:m1443
  45. Bullard J, Dust K, Funk D, Strong JE, Alexander D, Garnett L, Boodman C, Bello A, Hedley A, Schiffman Z, Doan K, Bastien N, Li Y, Van Caesele PG, Poliquin G: Predicting infectious severe acute respiratory syndrome coronavirus 2 from diagnostic samples. *Clin Infect Dis* 2020, 71:2663–2666
  46. Cevik M, Kuppalli K, Kindrachuk J, Peiris M: Virology, transmission, and pathogenesis of SARS-CoV-2. *BMJ* 2020, 371:m3862
  47. Hoorfar J, Malorny B, Abdulmawjood A, Cook N, Wagner M, Fach P: Practical considerations in design of internal amplification controls for diagnostic PCR assays. *J Clin Microbiol* 2004, 42:1863–1868
  48. Petter E, Mor O, Zuckerman N, Oz-Levi D, Younger A, Aran D, Erlich Y: Initial real world evidence for lower viral load of individuals who have been vaccinated by BNT162b2. *medRxiv* 2021, [Preprint] doi: 10.1101/2021.02.08.21251329
  49. Levine-Tiefenbrun M, Yelin I, Katz R, Herzel E, Golan Z, Schreiber L, Wolf T, Nadler V, Ben-Tov A, Kuint J, Gazit S, Patalon T, Chodick G, Kishony R: Initial report of decreased SARS-CoV-2 viral load after inoculation with the BNT162b2 vaccine. *Nat Med* 2021, 27:790–792